

=====

Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu Sep 20 16:11:22 EDT 2007

=====

Application No: 10518072 Version No: 1.0

Input Set:**Output Set:**

Started: 2007-09-10 15:56:40.626
Finished: 2007-09-10 15:56:48.761
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 135 ms
Total Warnings: 103
Total Errors: 121
No. of SeqIDs Defined: 129
Actual SeqID Count: 129

Error code	Error Description
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (5)

Input Set:

Output Set:

Started: 2007-09-10 15:56:40.626
Finished: 2007-09-10 15:56:48.761
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 135 ms
Total Warnings: 103
Total Errors: 121
No. of SeqIDs Defined: 129
Actual SeqID Count: 129

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (21)
W 402	Undefined organism found in <213> in SEQ ID (23)
W 402	Undefined organism found in <213> in SEQ ID (24)
W 402	Undefined organism found in <213> in SEQ ID (25)
W 402	Undefined organism found in <213> in SEQ ID (30)
W 402	Undefined organism found in <213> in SEQ ID (31)
W 402	Undefined organism found in <213> in SEQ ID (33)
W 402	Undefined organism found in <213> in SEQ ID (35)
W 402	Undefined organism found in <213> in SEQ ID (38)
W 213	Artificial or Unknown found in <213> in SEQ ID (39)
W 213	Artificial or Unknown found in <213> in SEQ ID (40)
W 213	Artificial or Unknown found in <213> in SEQ ID (41)
W 213	Artificial or Unknown found in <213> in SEQ ID (42)
W 213	Artificial or Unknown found in <213> in SEQ ID (43)

Input Set:

Output Set:

Started: 2007-09-10 15:56:40.626
Finished: 2007-09-10 15:56:48.761
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 135 ms
Total Warnings: 103
Total Errors: 121
No. of SeqIDs Defined: 129
Actual SeqID Count: 129

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (44)
W 213	Artificial or Unknown found in <213> in SEQ ID (45)
W 213	Artificial or Unknown found in <213> in SEQ ID (46)
W 213	Artificial or Unknown found in <213> in SEQ ID (47)
W 213	Artificial or Unknown found in <213> in SEQ ID (48)
W 213	Artificial or Unknown found in <213> in SEQ ID (49)
W 213	Artificial or Unknown found in <213> in SEQ ID (50)
W 213	Artificial or Unknown found in <213> in SEQ ID (54)
W 213	Artificial or Unknown found in <213> in SEQ ID (55)
W 402	Undefined organism found in <213> in SEQ ID (56)
W 402	Undefined organism found in <213> in SEQ ID (57)
W 213	Artificial or Unknown found in <213> in SEQ ID (58)
W 213	Artificial or Unknown found in <213> in SEQ ID (59)
W 402	Undefined organism found in <213> in SEQ ID (60) This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (63)
E 300	Invalid codon found Phe SEQID (63) POS: 432
E 300	Invalid codon found Leu SEQID (63) POS: 435
E 300	Invalid codon found Phe SEQID (63) POS: 438
E 300	Invalid codon found Leu SEQID (63) POS: 441
E 300	Invalid codon found Gly SEQID (63) POS: 444
E 300	Invalid codon found Thr SEQID (63) POS: 447

Input Set:

Output Set:

Started: 2007-09-10 15:56:40.626

Finished: 2007-09-10 15:56:48.761

Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 135 ms

Total Warnings: 103

Total Errors: 121

No. of SeqIDs Defined: 129

Actual SeqID Count: 129

Error code	Error Description
E 300	Invalid codon found Pro SEQID (63) POS: 450
E 300	Invalid codon found Glu SEQID (63) POS: 453
E 300	Invalid codon found Ala SEQID (63) POS: 456
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (64)
E 300	Invalid codon found Pro SEQID (64) POS: 289
E 300	Invalid codon found Lys SEQID (64) POS: 292
E 300	Invalid codon found Asn SEQID (64) POS: 295
E 300	Invalid codon found Ala SEQID (64) POS: 298
E 300	Invalid codon found Ala SEQID (64) POS: 301
E 300	Invalid codon found Val SEQID (64) POS: 304
E 300	Invalid codon found Met SEQID (64) POS: 307
E 300	Invalid codon found Leu SEQID (64) POS: 310
E 300	Invalid codon found Trp SEQID (64) POS: 313
E 300	Invalid codon found Ile SEQID (64) POS: 316
E 300	Invalid codon found Phe SEQID (64) POS: 319 This error has occurred more than 20 times, will not be displayed
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the

Input Set:

Output Set:

Started: 2007-09-10 15:56:40.626
Finished: 2007-09-10 15:56:48.761
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 135 ms
Total Warnings: 103
Total Errors: 121
No. of SeqIDs Defined: 129
Actual SeqID Count: 129

Error code	Error Description
E 321	No. of Bases conflict, this line has no nucleotides SEQID (78)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (83)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (97)
W 213	Artificial or Unknown found in <213> in SEQ ID (123)
W 213	Artificial or Unknown found in <213> in SEQ ID (124)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (125)
W 213	Artificial or Unknown found in <213> in SEQ ID (128)
W 213	Artificial or Unknown found in <213> in SEQ ID (129) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Weill, Mylene
Fort, Philippe
Raymond, Michel
Pasteur, Nicole

<120> NOVEL ACETYLCHOLINESTERASE GENE RESPONSIBLE FOR
INSECTICIDE RESISTANCE AND APPLICATIONS THEREOF

<130> 263365US0XPCT

<140> 10518072

<141> 2007-09-10

<150> FR 02/07622

<151> 2002-06-20

<150> FR 02/13799

<151> 2002-11-05

<160> 129

<170> PatentIn version 2.1

<210> 1

<211> 524

<212> PRT

<213> Anopheles gambiae

<400> 1

Asp	Pro	Leu	Val	Val	Asn	Thr	Asp	Lys	Gly	Arg	Ile	Arg	Gly	Ile	Thr
1				5					10					15	

Val	Asp	Ala	Pro	Ser	Gly	Lys	Lys	Val	Asp	Val	Trp	Leu	Gly	Ile	Pro
			20					25					30		

Tyr	Ala	Gln	Pro	Pro	Val	Gly	Pro	Leu	Arg	Phe	Arg	His	Pro	Arg	Pro
		35					40					45			

Ala	Glu	Lys	Trp	Thr	Gly	Val	Leu	Asn	Thr	Thr	Thr	Pro	Pro	Asn	Ser
	50					55					60				

Cys	Val	Gln	Ile	Val	Asp	Thr	Val	Phe	Gly	Asp	Phe	Pro	Gly	Ala	Thr
65					70					75				80	

Met	Trp	Asn	Pro	Asn	Thr	Pro	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Ile	Asn
				85						90				95	

Val	Val	Ala	Pro	Arg	Pro	Arg	Pro	Lys	Asn	Ala	Ala	Val	Met	Leu	Trp
			100					105					110		

Ile	Phe	Gly	Gly	Gly	Phe	Tyr	Ser	Gly	Thr	Ala	Thr	Leu	Asp	Val	Tyr
		115					120						125		

Asp	His	Arg	Ala	Leu	Ala	Ser	Glu	Glu	Asn	Val	Ile	Val	Val	Ser	Leu	130	135	140	
Gln	Tyr	Arg	Val	Ala	Ser	Leu	Gly	Phe	Leu	Phe	Leu	Gly	Thr	Pro	Glu	145	150	155	160
Ala	Pro	Gly	Asn	Ala	Gly	Leu	Phe	Asp	Gln	Asn	Leu	Ala	Leu	Arg	Trp	165	170	175	
Val	Arg	Asp	Asn	Ile	His	Arg	Phe	Gly	Gly	Asp	Pro	Ser	Arg	Val	Thr	180	185	190	
Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Val	Ser	Val	Ser	Leu	His	Leu	Leu	195	200	205	
Ser	Ala	Leu	Ser	Arg	Asp	Leu	Phe	Gln	Arg	Ala	Ile	Leu	Gln	Ser	Gly	210	215	220	
Ser	Pro	Thr	Ala	Pro	Trp	Ala	Leu	Val	Ser	Arg	Glu	Glu	Ala	Thr	Leu	225	230	235	240
Arg	Ala	Leu	Arg	Leu	Ala	Glu	Ala	Val	Gly	Cys	Pro	His	Glu	Pro	Ser	245	250	255	
Lys	Leu	Ser	Asp	Ala	Val	Glu	Cys	Leu	Arg	Gly	Lys	Asp	Pro	His	Val	260	265	270	
Leu	Val	Asn	Asn	Glu	Trp	Gly	Thr	Leu	Gly	Ile	Cys	Glu	Phe	Pro	Phe	275	280	285	
Val	Pro	Val	Val	Asp	Gly	Ala	Phe	Leu	Asp	Glu	Thr	Pro	Gln	Arg	Ser	290	295	300	
Leu	Ala	Ser	Gly	Arg	Phe	Lys	Lys	Thr	Glu	Ile	Leu	Thr	Gly	Ser	Asn	305	310	315	320
Thr	Glu	Glu	Gly	Tyr	Tyr	Phe	Ile	Ile	Tyr	Tyr	Leu	Thr	Glu	Leu	Leu	325	330	335	
Arg	Lys	Glu	Glu	Gly	Val	Thr	Val	Thr	Arg	Glu	Glu	Phe	Leu	Gln	Ala	340	345	350	
Val	Arg	Glu	Leu	Asn	Pro	Tyr	Val	Asn	Gly	Ala	Ala	Arg	Gln	Ala	Ile	355	360	365	
Val	Phe	Glu	Tyr	Thr	Asp	Trp	Thr	Glu	Pro	Asp	Asn	Pro	Asn	Ser	Asn	370	375	380	
Arg	Asp	Ala	Leu	Asp	Lys	Met	Val	Gly	Asp	Tyr	His	Phe	Thr	Cys	Asn	385	390	395	400
Val	Asn	Glu	Phe	Ala	Gln	Arg	Tyr	Ala	Glu	Glu	Gly	Asn	Asn	Val	Tyr	405	410	415	
Met	Tyr	Leu	Tyr	Thr	His	Arg	Ser	Lys	Gly	Asn	Pro	Trp	Pro	Arg	Trp	420	425	430	

Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr Val Phe Gly Glu Pro
435 440 445

Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp Glu Lys Asp Phe Ser Arg
450 455 460

Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys Thr Gly Asn Pro Asn
465 470 475 480

Pro Asn Thr Ala Ser Ser Glu Phe Pro Glu Trp Pro Lys His Thr Ala
485 490 495

His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn Thr Ser Phe Val Gly
500 505 510

Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp Lys
515 520

<210> 2

<211> 1932

<212> DNA

<213> Anopheles gambiae

<220>

<221> CDS

<222> (1)..(1932)

<400> 2

atg ttt gtg tgt tgt ttt ttc ttt ctc tct ctc tct ttc tgt ggt tcc 48
Met Phe Val Cys Cys Phe Phe Phe Leu Ser Leu Ser Phe Cys Gly Ser
1 5 10 15

aac att tca gac gca ttt ttt aca cca tat ata ggt cac ggt gag tcc 96
Asn Ile Ser Asp Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Glu Ser
20 25 30

gta cga att ata gat gcc gag ttg ggc acg ctc gag cat gtc cac agt 144
Val Arg Ile Ile Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser
35 40 45

gga gca acg ccg cgg cga cgc ggc ctg acg agg cgc gag tca aac tcg 192
Gly Ala Thr Pro Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser
50 55 60

gac gcg aac gac aac gat ccg ctg gtg gtc aac acg gat aag ggg cgc 240
Asp Ala Asn Asp Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg
65 70 75 80

atc cgc ggc att acg gtc gat gcg ccc agc ggc aag aag gtg gac gtg 288
Ile Arg Gly Ile Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val
85 90 95

tgg ctc ggc att ccc tac gcc cag ccg ccg gtc ggg ccg cta cgg ttc 336
Trp Leu Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe

100	105	110	
cgt cat ccg cgg ccg gcc gaa aag tgg acc ggc gtg ctg aac acg acc			384
Arg His Pro Arg Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr			
115	120	125	
aca ccg ccc aac agc tgc gtg cag atc gtg gac acc gtg ttc ggc gac			432
Thr Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp			
130	135	140	
ttc ccg ggc gcg acc atg tgg aac ccg aac acg ccc ctg tcc gag gac			480
Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp			
145	150	155	160
tgt ctg tac att aac gtg gtg gca ccg cga ccc cgg ccc aag aat gcg			528
Cys Leu Tyr Ile Asn Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala			
165	170	175	
gcc gtc atg ctg tgg atc ttc ggc ggc ggc ttc tac tcc ggc acc gcc			576
Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala			
180	185	190	
acc ctg gac gtg tac gac cac ccg gcg ctt gcg tcg gag gag aac gtg			624
Thr Leu Asp Val Tyr Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val			
195	200	205	
atc gtg gtg tcg ctg cag tac cgc gtg gcc agt ctg ggc ttc ctg ttt			672
Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe			
210	215	220	
ctc ggc acc ccg gaa gcg ccg ggc aat gcg gga ctg ttc gat cag aac			720
Leu Gly Thr Pro Glu Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn			
225	230	235	240
ctt gcg cta cgc tgg gtg ccg gac aac att cac ccg ttc ggt ggc gat			768
Leu Ala Leu Arg Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp			
245	250	255	
ccg tcg cgt gtg aca ctg ttc ggc gag agt gcc ggt gcc gtc tcg gtg			816
Pro Ser Arg Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val			
260	265	270	
tcg ctg cat ctg ctg tcc gcc ctt tcc cgc gat ctg ttc cag cgg gcc			864
Ser Leu His Leu Leu Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala			
275	280	285	
atc ctg cag agc ggc tcg ccg acg gca ccg tgg gca ttg gta tcg cgc			912
Ile Leu Gln Ser Gly Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg			
290	295	300	
gag gaa gcc aca cta aga gca ctg ccg ttg gcc gag gcg gtc ggc tgc			960
Glu Glu Ala Thr Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys			
305	310	315	320
ccg cac gaa ccg agc aag ctg agc gat gcg gtc gag tgc ctg cgc ggc			1008
Pro His Glu Pro Ser Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly			

325	330	335	
aag gac ccg cac gtg ctg gtc aac aac gag tgg ggc acg ctc ggc att			1056
Lys Asp Pro His Val Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile			
340	345	350	
tgc gag ttc ccg ttc gtg ccg gtg gtc gac ggt gcg ttc ctg gac gag			1104
Cys Glu Phe Pro Phe Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu			
355	360	365	
acg ccg cag cgt tcg ctc gcc agc ggg cgc ttc aag aag acg gag atc			1152
Thr Pro Gln Arg Ser Leu Ala Ser Gly Arg Phe Lys Lys Thr Glu Ile			
370	375	380	
ctc acc ggc agc aac acg gag gag ggc tac tac ttc atc atc tac tac			1200
Leu Thr Gly Ser Asn Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr			
385	390	395	400
ctg acc gag ctg ctg cgc aag gag gag ggc gtg acc gtg acg cgc gag			1248
Leu Thr Glu Leu Leu Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu			
405	410	415	
gag ttc ctg cag gcg gtg cgc gag ctc aac ccg tac gtg aac ggg gcg			1296
Glu Phe Leu Gln Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala			
420	425	430	
gcc ccg cag gcg atc gtg ttc gag tac acc gac tgg acc gag ccg gac			1344
Ala Arg Gln Ala Ile Val Phe Glu Tyr Thr Asp Trp Thr Glu Pro Asp			
435	440	445	
aac ccg aac agc aac cgg gac gcg ctg gac aag atg gtg ggc gac tat			1392
Asn Pro Asn Ser Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr			
450	455	460	
cac ttc acc tgc aac gtg aac gag ttc gcg cag ccg tac gcc gag gag			1440
His Phe Thr Cys Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu			
465	470	475	480
ggc aac aac gtc tac atg tat ctg tac acg cac cgc agc aaa ggc aac			1488
Gly Asn Asn Val Tyr Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn			
485	490	495	
ccg tgg ccg cgc tgg acg ggc gtg atg cac ggc gac gag atc aac tac			1536
Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr			
500	505	510	
gtg ttc ggc gaa ccg ctc aac ccc acc ctc ggc tac acc gag gac gag			1584
Val Phe Gly Glu Pro Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp Glu			
515	520	525	
aaa gac ttt agc cgg aag atc atg cga tac tgg tcc aac ttt gcc aaa			1632
Lys Asp Phe Ser Arg Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys			
530	535	540	
acc ggg aat cca aat ccc aac acg gcc agc agc gaa ttc ccc gag tgg			1680
Thr Gly Asn Pro Asn Pro Asn Thr Ala Ser Ser Glu Phe Pro Glu Trp			
545	550	555	560

ccc aag cac acc gcc cac gga cgg cac tat ctg gag ctg ggc ctc aac 1728
Pro Lys His Thr Ala His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn
565 570 575

acg tcc ttc gtc ggt cgg ggc cca cgg ttg agg cag tgt gcc ttc tgg 1776
Thr Ser Phe Val Gly Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp
580 585 590

aag aag tac ctt ccc cag cta gtt gca gct acc tcg aac cta cca ggg 1824
Lys Lys Tyr Leu Pro Gln Leu Val Ala Ala Thr Ser Asn Leu Pro Gly
595 600 605

cca gca ccg cct agt gaa ccg tgc gaa agc agc gca ttt ttt tac cga 1872
Pro Ala Pro Pro Ser Glu Pro Cys Glu Ser Ser Ala Phe Phe Tyr Arg
610 615 620

cct gat ctg atc gtg ctg ctg gtg tgc ctg ctt acg gcg acc gtc aga 1920
Pro Asp Leu Ile Val Leu Leu Val Ser Leu Leu Thr Ala Thr Val Arg
625 630 635 640

ttc ata caa taa 1932
Phe Ile Gln

<210> 3
<211> 643
<212> PRT
<213> Anopheles gambiae

<400> 3
Met Phe Val Cys Cys Phe Phe Phe Leu Ser Leu Ser Phe Cys Gly Ser
1 5 10 15

Asn Ile Ser Asp Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Glu Ser
20 25 30

Val Arg Ile Ile Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser
35 40 45

Gly Ala Thr Pro Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser
50 55 60

Asp Ala Asn Asp Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg
65 70 75 80

Ile Arg Gly Ile Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val
85 90 95

Trp Leu Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe
100 105 110

Arg His Pro Arg Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr
115 120 125

Thr Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp

130		135		140	
Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp					
145		150		155	160
Cys Leu Tyr Ile Asn Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala					
	165		170		175
Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala					
	180		185		190
Thr Leu Asp Val Tyr Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val					
	195		200		205
Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe					
	210		215		220
Leu Gly Thr Pro Glu Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn					
225		230		235	240
Leu Ala Leu Arg Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp					
	245		250		255
Pro Ser Arg Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val					
	260		265		270
Ser Leu His Leu Leu Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala					
	275		280		285
Ile Leu Gln Ser Gly Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg					
	290		295		300
Glu Glu Ala Thr Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys					
305		310		315	320
Pro His Glu Pro Ser Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly					
	325		330		335
Lys Asp Pro His Val Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile					
	340		345		350
Cys Glu Phe Pro Phe Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu					
	355		360		365
Thr Pro Gln Arg Ser Leu Ala Ser Gly Arg Phe Lys Lys Thr Glu Ile					
	370		375		380
Leu Thr Gly Ser Asn Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr					
385		390		395	400
Leu Thr Glu Leu Leu Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu					
	405		410		415
Glu Phe Leu Gln Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala					
	420		425		430

Ala Arg Gln Ala Ile Val Phe Glu Tyr Thr Asp Trp Thr Glu Pro Asp
435 440 445

Asn Pro Asn Ser Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr
450 455 460

His Phe Thr Cys Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu
465 470 475 480

Gly Asn Asn Val Tyr Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn
485 490 495

Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr
500 505 510

Val Phe Gly Glu Pro Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp G